Fig. 1

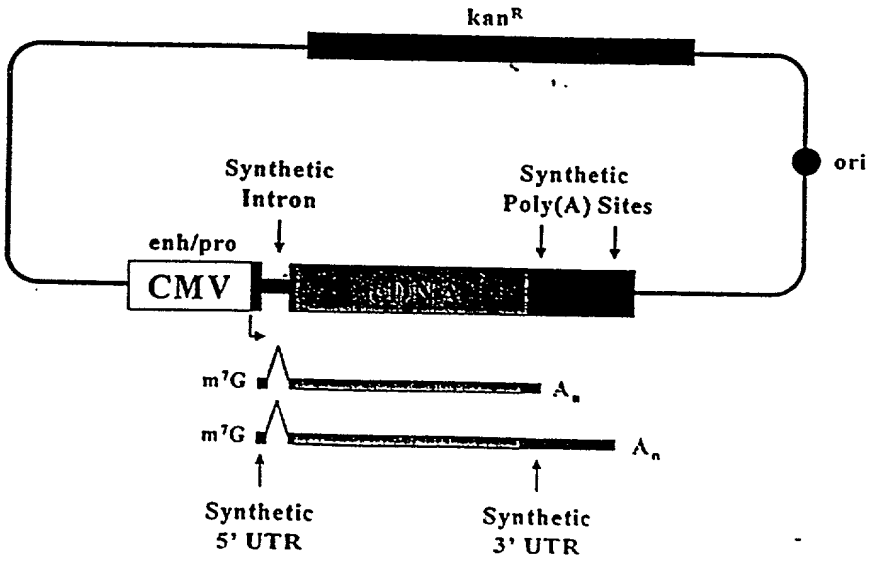
kan^R
ori
Synthetic
Intron
Synthetic
Poly(A) Sites
enh/pro
CMV
m7G
A_n
m7G
A_n
Synthetic
5' UTR
Synthetic
3' UTR

Fig. 2

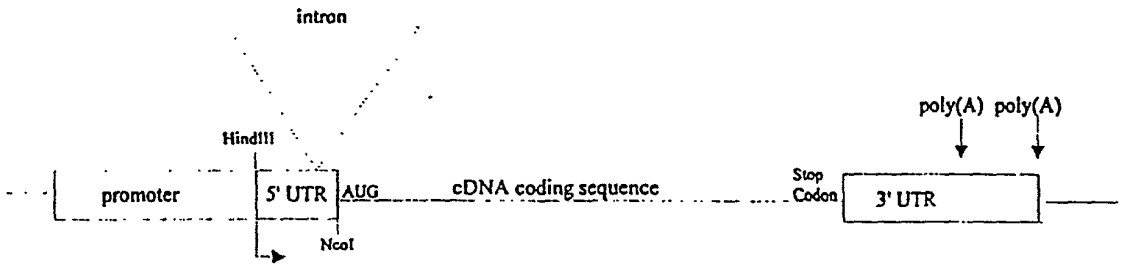
intron
poly(A) poly(A)
HindIII
promoter
5' UTR
AUG
cDNA coding sequence
Stop Codon
3' UTR
NcoI

Fig. 3

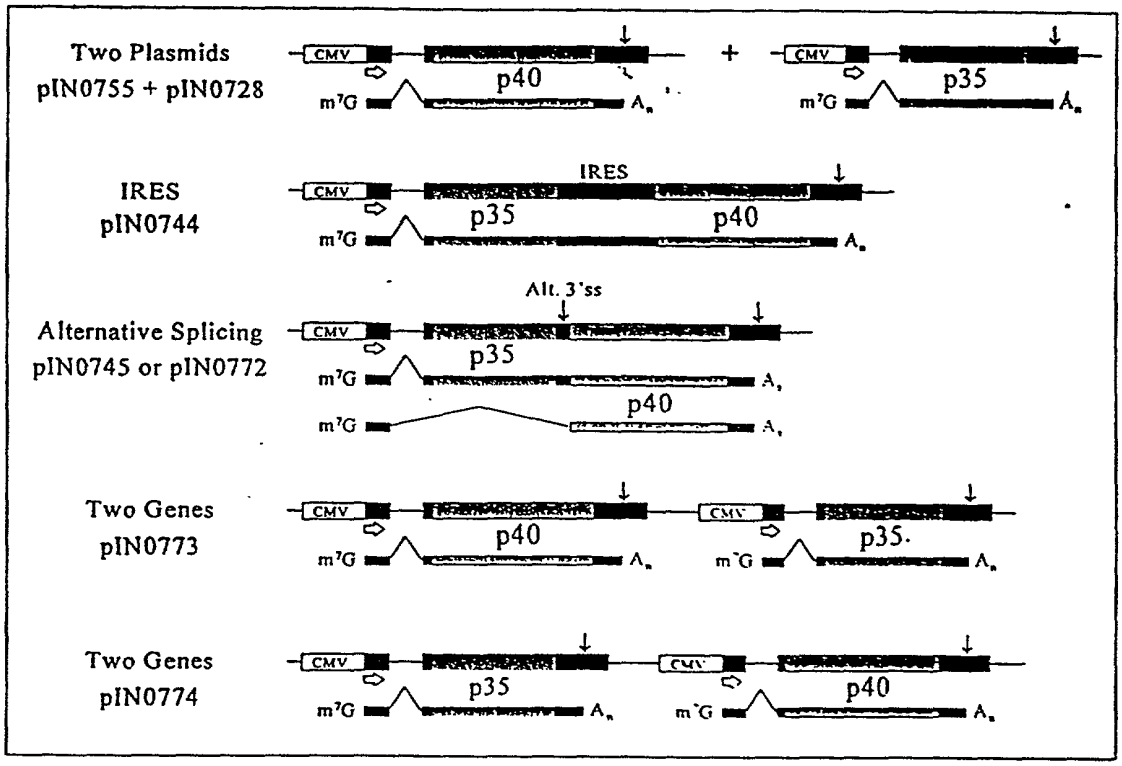
Two Plasmids
pIN0755 + pIN0728
CMV
p40
m7G
An
+
CMV
p35
m7G
An
IRES
pIN0744
CMV
IRES
p35
p40
m7G
An
Alternative Splicing
pIN0745 or pIN0772
Alt. 3'ss
CMV
p35
m7G
An
p40
m7G
An
Two Genes
pIN0773
CMV
p40
m7G
An
CMV
p35.
m7G
An
Two Genes
pIN0774
CMV
p35
m7G
An
CMV
p40
m7G
An

Fig. 4A

File : H40.AMI
Range : 1 - 329
Codon Table : Universal

SEQ ID NO. 1

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                                                10                                                  20
Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu Ala Ser Pro Leu
ATG TGY CAY CAR CAR YTN GTN ATH WSN TGG TTY WSN YTN GTN TTY YTN GCN WSN CCN YTN
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
ATG TGT CAT CAA CAA TTA GTT ATT TCT TGG TTT TCT TTA GTT TTT TTA GCT TCT CCT TTA
    TGC CAC CAG CAG TTG GTC ATC TCC     TTC TCC TTG GTC TTC TTG GCC TCC CCC TTG
                   CTT GTA ATA TCA         TCA CTT GTA     CTT GCA TCA CCA CTT
                   CTC GTG     TCG         TCG CTC GTG     CTC GCG TCG CCG CTC
                   CTA         AGT         AGT CTA         CTA     AGT     CTA
                   CTG         AGC         AGC CTG         CTG     AGC     CTG

                                            30                                                  40
Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr Pro Asp
GTN GCN ATH TGG GAR YTN AAR AAR GAY GTN TAY GTN GTN GAR YTN GAY TGG TAY CCN GAY
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
GTT GCT ATT TGG GAA TTA AAA AAA GAT GTT TAT GTT GTT GAA TTA GAT TGG TAT CCT GAT
GTC GCC ATC     GAG TTG AAG AAG GAC GTC TAC GTC GTC GAG TTG GAC     TAC CCC GAC
GTA GCA ATA         CTT             GTA     GTA GTA     CTT             CCA
GTG GCG             CTC             GTG     GTG GTG     CTC             CCG
                    CTA                                 CTA
                    CTG                                 CTG

                                            50                                                  60
Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp
GCN CCN GGN GAR ATG GTN GTN YTN ACN TGY GAY ACN CCN GAR GAR GAY GGN ATH ACN TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
GCT CCT GGT GAA ATG GTT GTT TTA ACT TGT GAT ACT CCT GAA GAA GAT GGT ATT ACT TGG
GCC CCC GGC GAG     GTC GTC TTG ACC TGC GAC ACC CCC GAG GAG GAC GGC ATC ACC
GCA CCA GGA         GTA GTA CTT ACA         ACA CCA             GGA ATA ACA
GCG CCG GGG         GTG GTG CTC ACG         ACG CCG             GGG     ACG
                            CTA
                            CTG

                                            70                                                  80
Thr Leu Asp Gln Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
ACN YTN GAY CAR WSN WSN GAR GTN YTN GGN WSN GGN AAR ACN YTN ACN ATH CAR GTN AAR
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
ACT TTA GAT CAA TCT TCT GAA GTT TTA GGT TCT GGT AAA ACT TTA ACT ATT CAA GTT AAA
ACC TTG GAC CAG TCC TCC GAG GTC TTG GGC TCC GGC AAG ACC TTG ACC ATC CAG GTC AAG
ACA CTT         TCA TCA     GTA CTT GGA TCA GGA     ACA CTT ACA ATA     GTA
ACG CTC         TCG TCG     GTG CTC GGG TCG GGG     ACG CTC ACG         GTG
    CTA         AGT AGT         CTA     AGT             CTA
    CTG         AGC AGC         CTG     AGC             CTG

                                            90                                                  100
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser
GAR TTY GGN GAY GCN GGN CAR TAY ACN TGY CAY AAR GGN GGN GAR GTN YTN WSN CAY WSN
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
GAA TTT GGT GAT GCT GGT CAA TAT ACT TGT CAT AAA GGT GGT GAA GTT TTA TCT CAT TCT
GAG TTC GGC GAC GCC GGC CAG TAC ACC TGC CAC AAG GGC GGC GAG GTC TTG TCC CAC TCC
        GGA     GCA GGA         ACA             GGA GGA     GTA CTT TCA     TCA
        GGG     GCG GGG         ACG             GGG GGG     GTG CTC TCG     TCG
                                                                CTA AGT     AGT
                                                                CTG AGC     AGC
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Fig. 4B

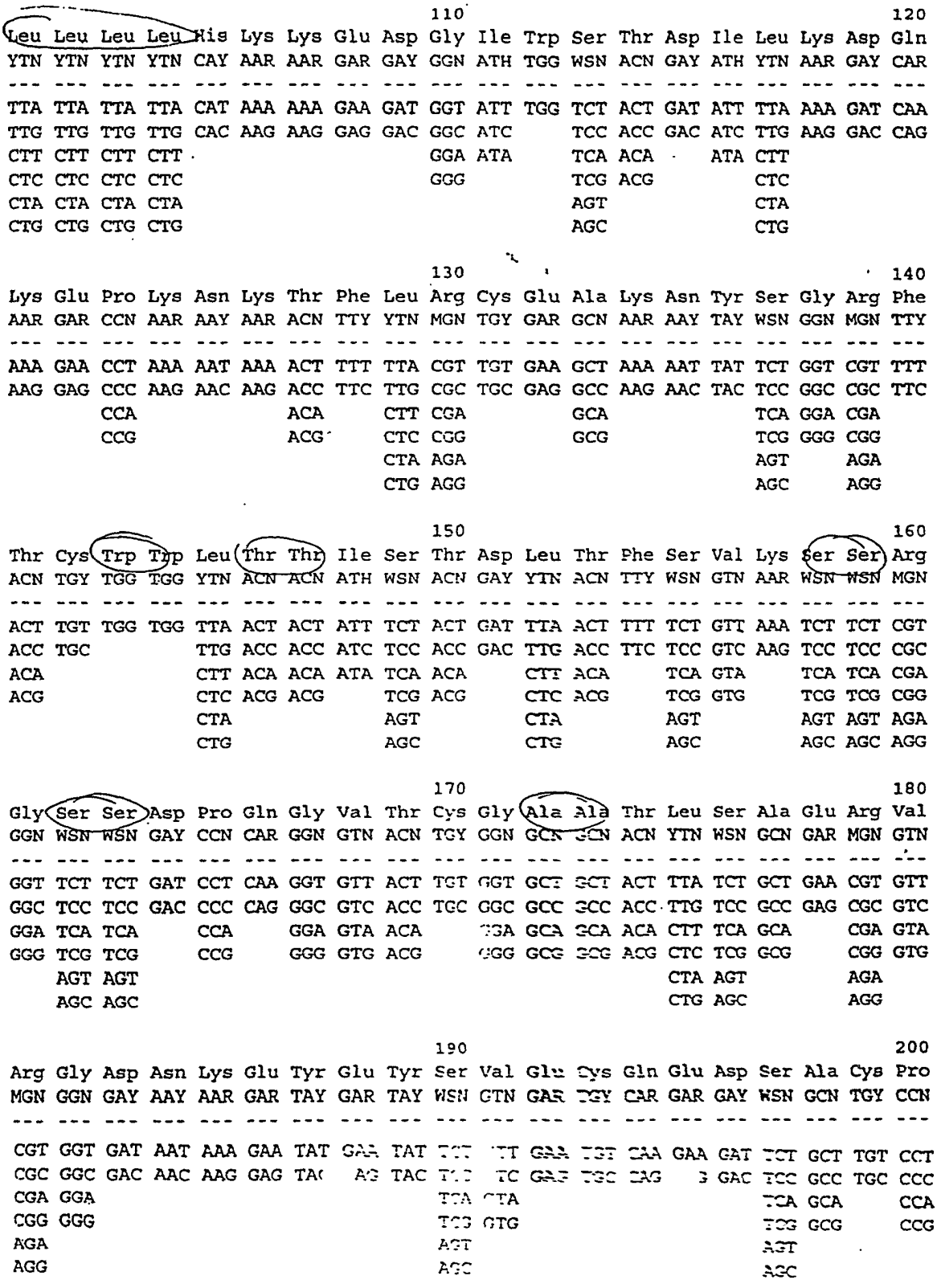
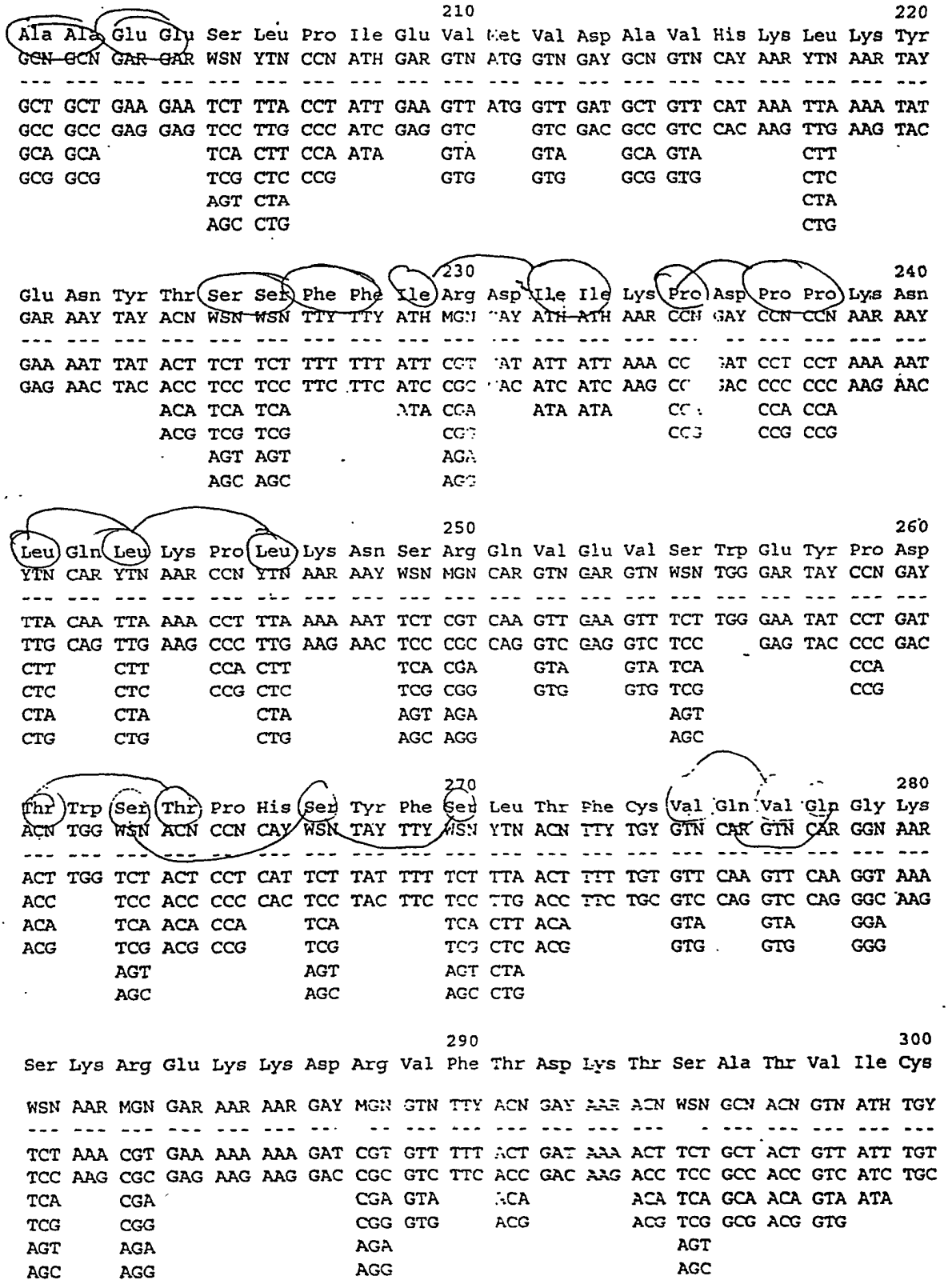

110 120
Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys Asp Gln
YTN YTN YTN YTN CAY AAR AAR GAR GAY GGN ATH TGG WSN ACN GAY ATH YTN AAR GAY CAR
TTA TTA TTA TTA CAT AAA AAA GAA GAT GGT ATT TGG TCT ACT GAT ATT TTA AAA GAT CAA
TTG TTG TTG TTG CAC AAG AAG GAG GAC GGC ATC TCC ACC GAC ATC TTG AAG GAC CAG
CTT CTT CTT CTT GGA ATA TCA ACA ATA CTT
CTC CTC CTC CTC GGG TCG ACG CTC
CTA CTA CTA CTA AGT CTA
CTG CTG CTG CTG AGC CTG
130 140
Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe
AAR GAR CCN AAR AAY AAR ACN TTY YTN MGN TGY GAR GCN AAR AAY TAY WSN GGN MGN TTY
AAA GAA CCT AAA AAT AAA ACT TTT TTA CGT TGT GAA GCT AAA AAT TAT TCT GGT CGT TTT
AAG GAG CCC AAG AAC AAG ACC TTC TTG CGC TGC GAG GCC AAG AAC TAC TCC GGC CGC TTC
CCA ACA CTT CGA GCA TCA GGA CGA
CCG ACG CTC CGG GCG TCG GGG CGG
CTA AGA AGT AGA
CTG AGG AGC AGG
150 160
Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg
ACN TGY TGG TGG YTN ACN ACN ATH WSN ACN GAY YTN ACN TTY WSN GTN AAR WSN WSN MGN
ACT TGT TGG TGG TTA ACT ACT ATT TCT ACT GAT TTA ACT TTT TCT GTT AAA TCT TCT CGT
ACC TGC TTG ACC ACC ATC TCC ACC GAC TTG ACC TTC TCC GTC AAG TCC TCC CGC
ACA CTT ACA ACA ATA TCA ACA CTT ACA TCA GTA TCA TCA CGA
ACG CTC ACG ACG TCG ACG CTC ACG TCG GTG TCG TCG CGG
CTA AGT CTA AGT AGT AGA
CTG AGC CTG AGC AGC AGG
170 180
Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val
GGN WSN WSN GAY CCN CAR GGN GTN ACN TGY GGN GCN GCN ACN YTN WSN GCN GAR MGN GTN
GGT TCT TCT GAT CCT CAA GGT GTT ACT TGT GGT GCT GCT ACT TTA TCT GCT GAA CGT GTT
GGC TCC TCC GAC CCC CAG GGC GTC ACC TGC GGC GCC GCC ACC TTG TCC GCC GAG CGC GTC
GGA TCA TCA CCA GGA GTA ACA TGA GCA GCA ACA CTT TCA GCA CGA GTA
GGG TCG TCG CCG GGG GTG ACG GGG GCG GCG ACG CTC TCG GCG CGG GTG
AGT AGT CTA AGT AGA
AGC AGC CTG AGC AGG
190 200
Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala Cys Pro
MGN GGN GAY AAY AAR GAR TAY GAR TAY WSN GTN GAR TGY CAR GAR GAY WSN GCN TGY CCN
CGT GGT GAT AAT AAA GAA TAT GAA TAT TCT GTT GAA TGT CAA GAA GAT TCT GCT TGT CCT
CGC GGC GAC AAC AAG GAG TAC AGT TAC TCC GTC GAG TGC CAG GAC TCC GCC TGC CCC
CGA GGA TCA CTA TCA GCA CCA
CGG GGG TCG GTG TCG GCG CCG
AGA AGT AGT
AGG AGC AGC

Fig. 4C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GCT GCT GAA GAA TCT TTA CCT ATT GAA GTT ATG GTT GAT GCT GTT CAT AAA TTA AAA TAT
GCC GCC GAG GAG TCC TTG CCC ATC GAG GTC GTC GAC GCC GTC CAC AAG TTG AAG TAC
GCA GCA TCA CTT CCA ATA GTA GTA GCA GTA CTT
GCG GCG TCG CTC CCG GTG GTG GCG GTG CTC
AGT CTA CTA
AGC CTG CTG
230 240
Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
GAR AAY TAY ACN WSN WSN TTY TTY ATH MGN GAY ATH ATH AAR CCN GAY CCN CCN AAR AAY
GAA AAT TAT ACT TCT TCT TTT TTT ATT CGT GAT ATT ATT AAA CC GAT CCT CCT AAA AAT
GAG AAC TAC ACC TCC TCC TTC TTC ATC CGC GAC ATC ATC AAG CC GAC CCC CCC AAG AAC
ACA TCA TCA ATA CGA ATA ATA CC CCA CCA
ACG TCG TCG CGT CCG CCG CCG
AGT AGT AGA
AGC AGC AGG
250 260
Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp
YTN CAR YTN AAR CCN YTN AAR AAY WSN MGN CAR GTN GAR GTN WSN TGG GAR TAY CCN GAY
TTA CAA TTA AAA CCT TTA AAA AAT TCT CGT CAA GTT GAA GTT TCT TGG GAA TAT CCT GAT
TTG CAG TTG AAG CCC TTG AAG AAC TCC CGC CAG GTC GAG GTC TCC GAG TAC CCC GAC
CTT CTT CCA CTT TCA CGA GTA GTA TCA CCA
CTC CTC CCG CTC TCG CGG GTG GTG TCG CCG
CTA CTA CTA AGT AGA AGT
CTG CTG CTG AGC AGG AGC
270 280
Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln Gly Lys
ACN TGG WSN ACN CCN CAY WSN TAY TTY WSN YTN ACN TTY TGY GTN CAR GTN CAR GGN AAR
ACT TGG TCT ACT CCT CAT TCT TAT TTT TCT TTA ACT TTT TGT GTT CAA GTT CAA GGT AAA
ACC TCC ACC CCC CAC TCC TAC TTC TCC TTG ACC TTC TGC GTC CAG GTC CAG GGC AAG
ACA TCA ACA CCA TCA TCA CTT ACA GTA GTA GGA
ACG TCG ACG CCG TCG TCG CTC ACG GTG GTG GGG
AGT AGT AGT CTA
AGC AGC AGC CTG
290 300
Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys
WSN AAR MGN GAR AAR AAR GAY MGN GTN TTY ACN GAY AAR ACN WSN GCN ACN GTN ATH TGY
TCT AAA CGT GAA AAA AAA GAT CGT GTT TTT ACT GAT AAA ACT TCT GCT ACT GTT ATT TGT
TCC AAG CGC GAG AAG AAG GAC CGC GTC TTC ACC GAC AAG ACC TCC GCC ACC GTC ATC TGC
TCA CGA CGA GTA ACA ACA TCA GCA ACA GTA ATA
TCG CGG CGG GTG ACG ACG TCG GCG ACG GTG
AGT AGA AGA AGT
AGC AGG AGG AGC

Fig. 4D

									310										320
Arg	Lys	Asn	Ala	Ser	Ile	Ser	Val	Arg	Ala	Gln	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser
MGN	AAR	AAY	GCN	WSN	ATH	WSN	GTN	MGN	GCN	CAR	GAY	MGN	TAY	TAY	WSN	WSN	WSN	TGG	WSN
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
CGT	AAA	AAT	GCT	TCT	ATT	TCT	GTT	CGT	GCT	CAA	GAT	CGT	TAT	TAT	TCT	TCT	TCT	TGG	TCT
CGC	AAG	AAC	GCC	TCC	ATC	TCC	GTC	CGC	GCC	CAG	GAC	CGC	TAC	TAC	TCC	TCC	TCC		TCC
CGA			GCA	TCA	ATA	TCA	GTA	CGA	GCA			CGA			TCA	TCA	TCA		TCA
CGG			GCG	TCG		TCG	GTG	CGG	GCG			CGG			TCG	TCG	TCG		TCG
AGA				AGT		AGT		AGA				AGA			AGT	AGT	AGT		AGT
AGG				AGC		AGC		AGG				AGG			AGC	AGC	AGC		AGC

Glu	Trp	Ala	Ser	Val	Pro	Cys	Ser	***
GAR	TGG	GCN	WSN	GTN	CCN	TGY	WSN	TRR
---	---	---	---	---	---	---	---	---
GAA	TGG	GCT	TCT	GTT	CCT	TGT	TCT	TAA
GAG		GCC	TCC	GTC	CCC	TGC	TCC	TAG
		GCA	TCA	GTA	CCA		TCA	TGA
		GCG	TCG	GTG	CCG		TCG	
			AGT				AGT	
			AGC				AGC	

Fig. 5A

File : H35.AMI
Range : 1 - 220
Codon Table : Universal
SEQ ID NO. 5

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--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
ATG TGT CCT GCT CGT TCT TTA TTA TTA GTT GCT ACT TTA GTT TTA TTA GAT CAT TTA TCT
    TGC CCC GCC CGC TCC TTG TTG TTG GTC GCC ACC TTG GTC TTG TTG GAC CAC TTG TCC
        CCA GCA CGA TCA CTT CTT CTT GTA GCA ACA CTT GTA CTT CTT     CTT TCA
        CCG GCG CGG TCG CTC CTC CTC GTG GCG ACG CTC GTG CTC CTC     CTC TCG
                AGA AGT CTA CTA CTA         CTA   CTA CTA         CTA AGT
                AGG AGC CTG CTG CTG         CTG   CTG CTG         CTG AGC

                                                  30                                                  40
Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys Leu His His
YTN GCN MGN AAY YTN CCN GTN GCN ACN CCN GAY CCN GGN ATG TTY CCN TGY YTN CAY CAY
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
TTA GCT CGT AAT TTA CCT GTT GCT ACT CCT GAT CCT GGT ATG TTT CCT TGT TTA CAT CAT
TTG GCC CGC AAC TTG CCC GTC GCC ACC CCC GAC CCC GGC   TTC CCC TGC TTG CAC CAC
CTT GCA CGA   CTT CCA GTA GCA ACA CCA   CCA GGA       CCA   CTT
CTC GCG CGG   CTC CCG GTG GCG ACG CCG   CCG GGG       CCG   CTC
CTA   AGA     CTA                                           CTA
CTG   AGG     CTG                                           CTG

                                                  50                                                  60
Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu
WSN CAR AAY YTN YTN MGN GCN GTN WSN AAY ATG YTN CAR AAR GCN MGN CAR ACN YTN GAR
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
TCT CAA AAT TTA TTA CGT GCT GTT TCT AAT ATG TTA CAA AAA GCT CGT CAA ACT TTA GAA
TCC CAG AAC TTG TTG CGC GCC GTC TCC AAC   TTG CAG AAG GCC CGC CAG ACC TTG GAG
TCA       CTT CTT CGA GCA GTA TCA         CTT       GCA CGA     ACA CTT
TCG       CTC CTC CGG GCG GTG TCG         CTC       GCG CGG     ACG CTC
AGT       CTA CTA AGA       AGT           CTA             AGA         CTA
AGC       CTG CTG AGG       AGC           CTG             AGG         CTG

                                                  70                                                  80
Phe Tyr Pro Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
TTY TAY CCN TGY ACN WSN GAR GAR ATH GAY CAY GAR GAY ATH ACN AAR GAY AAR ACN WSN
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
TTT TAT CCT TGT ACT TCT GAA GAA ATT GAT CAT GAA GAT ATT ACT AAA GAT AAA ACT TCT
TTC TAC CCC TGC ACC TCC GAG GAG ATC GAC CAC GAG GAC ATC ACC AAG GAC AAG ACC TCC
    CCA   ACA TCA       ATA               ATA ACA           ACA TCA
    CCG   ACG TCG                         ACG               ACG TCG
              AGT                                           AGT
              AGC                                           AGC

                                                  90                                                  100
Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser Arg
ACN GTN GAR GCN TGY YTN CCN YTN GAR YTN ACN AAR AAY GAR WSN TGY YTN AAY WSN MGN
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
ACT GTT GAA GCT TGT TTA CCT TTA GAA TTA ACT AAA AAT GAA TCT TGT TTA AAT TCT CGT
ACC GTC GAG GCC TGC TTG CCC TTG GAG TTG ACC AAG AAC GAG TCC TGC TTG AAC TCC CGC
ACA GTA   GCA   CTT CCA CTT   CTT ACA       TCA   CTT   TCA CGA
ACG GTG   GCG   CTC CCC TC    CTC ACG       AGT   CTC   TCG CGG
                CTA   CTA     CTA           AGT   CTA   AGT AGA
                CTG   CTG     CTG           AGC   CTG   AGC AGG
```

Fig. 5B

```
                                                  110                                                 120
Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Met
GAR ACN WSN TTY ATH ACN AAY GGN WSN TGY YTN GCN WSN MGN AAR ACN WSN TTY ATG ATG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
GAA ACT TCT TTT ATT ACT AAT GGT TCT TGT TTA GCT TCT CGT AAA ACT TCT TTT ATG ATG
GAG ACC TCC TTC ATC ACC AAC GGC TCC TGC TTG GCC TCC CGC AAG ACC TCC TTC
    ACA TCA     ATA ACA     GGA TCA     CTT GCA TCA CGA     ACA TCA
    ACG TCG         ACG     GGG TCG     CTC GCG TCG CGG     ACG TCG
        AGT                     AGT     CTA     AGT AGA         AGT
        AGC                     AGC     CTG     AGC AGG         AGC

                                                  130                                                 140
Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr
GCN YTN TGY YTN WSN WSN ATH TAY GAR GAY YTN AAR ATG TAY CAR GTN GAR TTY AAR ACN
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
GCT TTA TGT TTA TCT TCT ATT TAT GAA GAT TTA AAA ATG TAT CAA GTT GAA TTT AAA ACT
GCC TTG TGC TTG TCC TCC ATC TAC GAG GAC TTG AAG     TAC CAG GTC GAG TTC AAG ACC
GCA CTT     CTT TCA TCA ATA             CTT                 GTA             ACA
GCG CTC     CTC TCG TCG                 CTC                 GTG             ACG
    CTA     CTA AGT AGT                 CTA
    CTG     CTG AGC AGC                 CTG

                                                  150                                                 160
Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
ATG AAY GCN AAR YTN YTN ATG GAY CCN AAR MGN CAR ATH TTY YTN GAY CAR AAY ATG YTN
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
ATG AAT GCT AAA TTA TTA ATG GAT CCT AAA CGT CAA ATT TTT TTA GAT CAA AAT ATG TTA
    AAC GCC AAG TTG TTG     GAC CCC AAG CGC CAG ATC TTC TTG GAC CAG AAC     TTG
        GCA     CTT CTT         CCA     CGA     ATA     CTT                 CTT
        GCG     CTC CTC         CCG     CGG             CTC                 CTC
                CTA CTA                 AGA             CTA                 CTA
                CTG CTG                 AGG             CTG                 CTG

                                                  170                                                 180
Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys
GCN GTN ATH GAY GAR YTN ATG CAR GCN YTN AAY TTY AAY WSN GAR ACN GTN CCN CAR AAR
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
GCT GTT ATT GAT GAA TTA ATG CAA GCT TTA AAT TTT AAT TCT GAA ACT GTT CCT CAA AAA
GCC GTC ATC GAC GAG TTG     CAG GCC TTG AAC TTC AAC TCC GAG ACC GTC CCC CAG AAG
GCA GTA ATA         CTT         GCA CTT             TCA     ACA GTA CCA
GCG GTG             CTC         GCG CTC             TCG     ACG GTG CCG
                    CTA             CTA             AGT
                    CTG             CTG             AGC

                                                  190                                                 200
Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His
WSN WSN YTN GAR GAR CCN GAY TTY TAY AAR ACN AAR ATH AAR YTN TGY ATH YTN YTN CAY
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

TCT TCT TTA GAA GAA CCT GAT TTT TAT AAA ACT AAA ATT AAA TTA TGT ATT TTA TTA CAT
TCC TCC TTG GAG GAG CCC GAC   TC TAC AAG ACC AAG ATC AAG   G TGC ATC TTG TTG CAC
TCA TCA CTT         CCA                 ACA     ATA     CTT     ATA CTT CTT
TCG TCG CTC         CCG                 ACG             CTC         CTC CTC
AGT AGT CTA                                             CTA         CTA CTA
AGC AGC CTG                                             CTG         CTG CTG
```

Fig. 5C

```
                                                  210                                                 220
Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Thr Ser Tyr Leu Asn Ala Ser ***
GCN TTY MGN ATH MGN GCN GTN ACN ATH GAY MGN GTN ACN WSN TAY YTN AAY GCN WSN TRR
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
GCT TTT CGT ATT CGT GCT GTT ACT ATT GAT CGT GTT ACT TCT TAT TTA AAT GCT TCT TAA
GCC TTC CGC ATC CGC GCC GTC ACC ATC GAC CGC GTC ACC TCC TAC TTG AAC GCC TCC TAG
GCA     CGA ATA CGA GCA GTA ACA ATA     CGA GTA ACA TCA     CTT     GCA TCA TGA
GCG     CGG     CGG GCG GTG ACG         CGG GTG ACG TCG     CTC     GCG TCG
        AGA     AGA                     AGA         AGT     CTA         AGT
        AGG     AGG                     AGG         AGC     CTG         AGC
```

Fig. 6

Codon Frequency Tables

human_high.cod

Codon usage for human (highly expressed) genes 1/24/91.

AmAcid	Codon	Number	/1000	Fraction
Gly	GGG	905.00	18.76	0.24
Gly	GGA	525.00	10.88	0.14
Gly	GGT	441.00	9.14	0.12
Gly	GGC	1867.00	38.70	0.50
Glu	GAG	2420.00	50.16	0.75
Glu	GAA	792.00	16.42	0.25
Asp	GAT	592.00	12.27	0.25
Asp	GAC	1821.00	37.73	0.75
Val	GTG	1866.00	38.68	0.66
Val	GTA	234.00	2.78	0.05
Val	GTT	198.00	4.10	0.07
Val	GTC	726.00	15.69	0.25
Ala	GCG	652.00	13.51	0.17
Ala	GCA	486.00	10.12	0.13
Ala	GCT	634.00	13.56	0.17
Ala	GCC	2057.00	42.64	0.53
Arg	AGG	512.00	10.61	0.18
Arg	AGA	294.00	6.18	0.10
Ser	AGT	354.00	7.34	0.16
Ser	AGC	1171.00	24.27	0.54
Lys	AAG	2117.00	43.88	0.82
Lys	AAA	471.00	9.76	0.18
Asn	AAT	314.00	6.51	0.22
Asn	AAC	1120.00	23.22	0.78
Met	ATG	1077.00	22.32	1.00
Ile	ATA	88.00	1.82	0.05
Ile	ATT	315.00	6.53	0.18
Ile	ATC	1368.00	28.38	0.77
Thr	ACG	405.00	8.40	0.15
Thr	ACA	373.00	7.73	0.14
Thr	ACT	358.00	7.42	0.14
Thr	ACC	1502.00	31.13	0.57
Trp	TGG	652.00	13.51	1.00
End	TGA	109.00	2.26	0.55
Cys	TGT	325.00	6.74	0.32
Cys	TGC	706.00	14.63	0.68
End	TAG	42.00	0.87	0.21
End	TAA	46.00	0.95	0.23
Tyr	TAT	360.00	7.46	0.26
Tyr	TAC	1042.00	21.60	0.74
Leu	TTG	313.00	6.49	0.06
Leu	TTA	76.00	1.58	0.02
Phe	TTT	336.00	6.96	0.20
Phe	TTC	1377.00	28.54	0.80
Ser	TCG	329.00	6.74	0.09
Ser	TCA	165.00	3.42	0.05
Ser	TCT	450.00	9.33	0.13
Ser	TCC	958.00	19.85	0.28
Arg	CGG	611.00	12.67	0.21
Arg	CGA	183.00	3.79	0.06
Arg	CGT	210.00	4.35	0.07
Arg	CGC	1086.00	22.51	0.37
Gln	CAG	2020.00	41.87	0.88
Gln	CAA	283.00	5.87	0.12
His	CAT	234.00	4.85	0.31
His	CAC	870.00	18.03	0.79
Leu	CTG	2884.00	59.78	0.44
Leu	CTA	166.00	3.44	0.03
Leu	CTT	238.00	4.93	0.05
Leu	CTC	1276.00	26.45	0.20
Pro	CCG	482.00	9.99	0.17
Pro	CCA	456.00	9.45	0.16
Pro	CCT	568.00	11.77	0.13
Pro	CCC	1418.00	29.22	0.44

Fig. 7

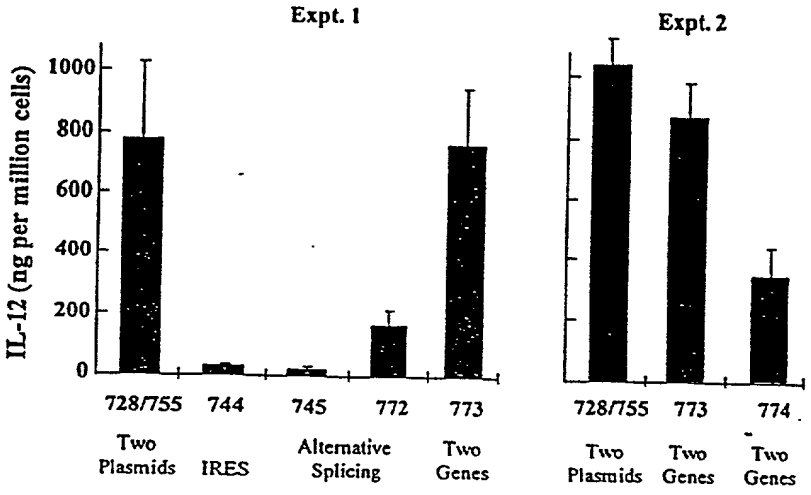

Expt. 1
Expt. 2
IL-12 (ng per million cells)
1000
800
600
400
200
0
728/755
744
745
772
773
774
Two Plasmids
IRES
Alternative Splicing
Two Genes
Two Plasmids
Two Genes
Two Genes

Fig. 8

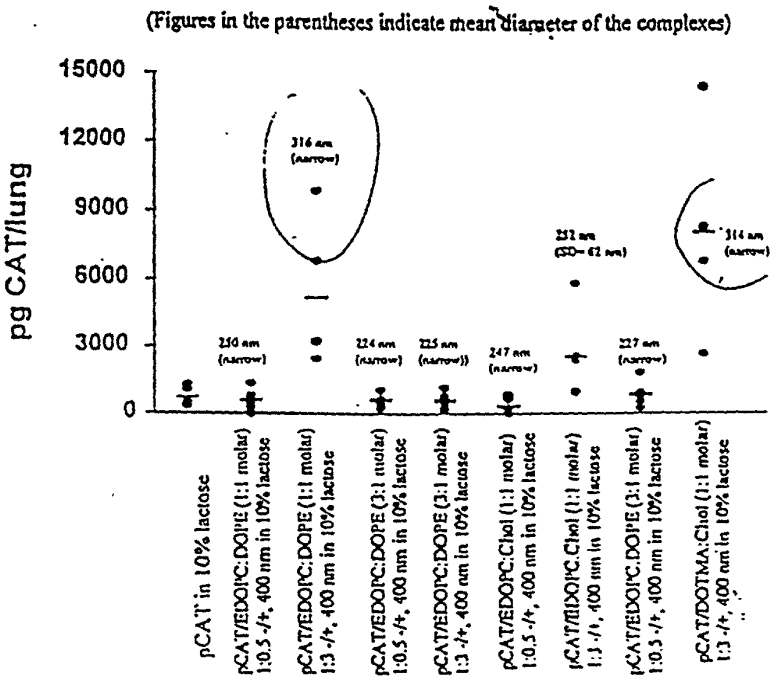
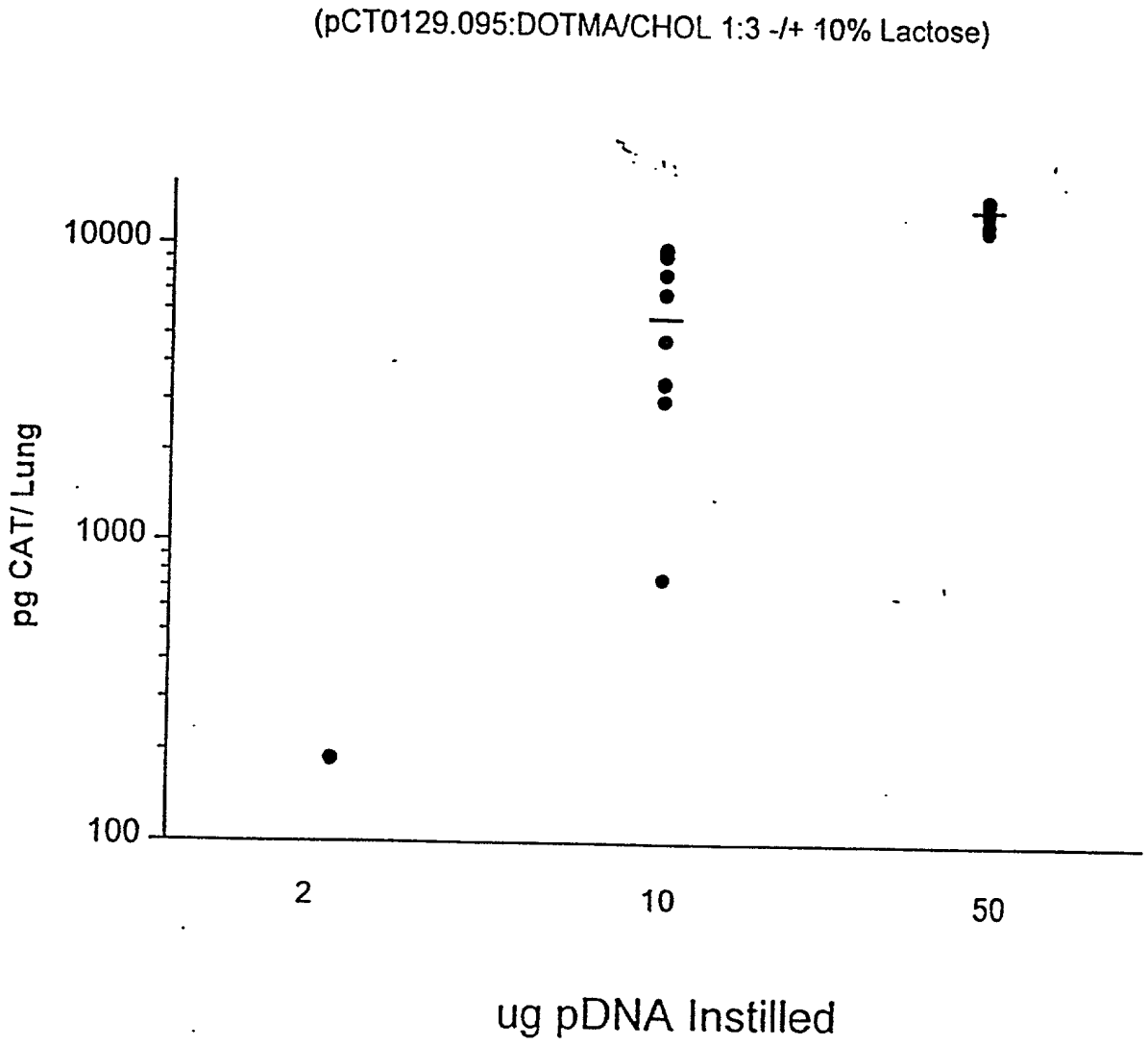

(Figures in the parentheses indicate mean diameter of the complexes)
pg CAT/lung
15000
12000
9000
6000
3000
0
316 nm (narrow)
250 nm (narrow)
224 nm (narrow)
225 nm (narrow))
247 nm (narrow)
227 nm (narrow)
314 nm (narrow)
pCAT in 10% lactose
pCAT/EDOPC:DOPE (1:1 molar) 1:0.5 -/+, 400 nm in 10% lactose
pCAT/EDOPC:DOPE (1:1 molar) 1:3 -/+, 400 nm in 10% lactose
pCAT/EDOPC:DOPE (3:1 molar) 1:0.5 -/+, 400 nm in 10% lactose
pCAT/EDOPC:DOPE (3:1 molar) 1:3 -/+, 400 nm in 10% lactose
pCAT/EDOPC:Chol (1:1 molar) 1:0.5 -/+, 400 nm in 10% lactose
pCAT/EDOPC:Chol (1:1 molar) 1:3 -/+, 400 nm in 10% lactose
pCAT/EDOPC:DOPE (3:1 molar) 1:0.5 -/+, 400 nm in 10% lactose
pCAT/DOTMA:Chol (1:1 molar) 1:3 -/+, 400 nm in 10% lactose

Fig. 9


(pCT0129.095:DOTMA/CHOL 1:3 -/+ 10% Lactose)
10000
1000
100
pg CAT/ Lung
2
10
50
ug pDNA Instilled

Antigen-Induced Airway Inflammation Model in Guinea Pigs

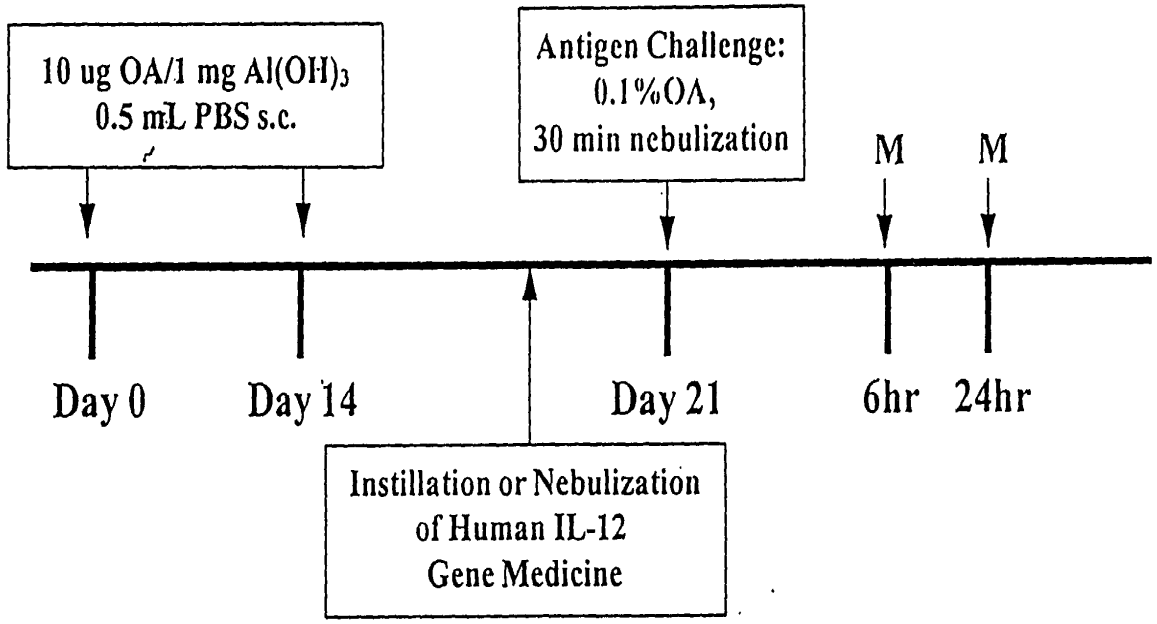
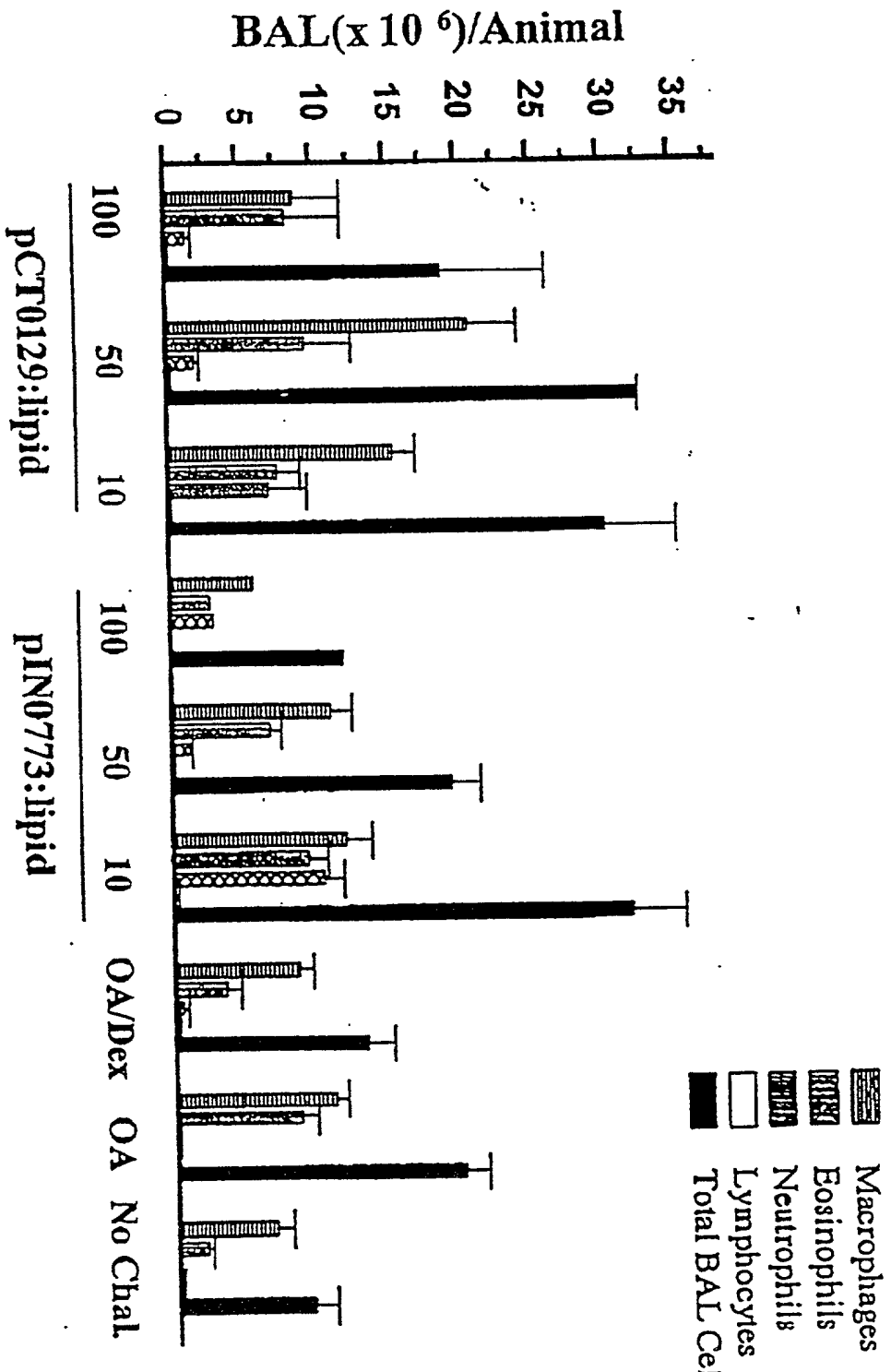


Fig. 10

M (measurement) = bronchoalveolar lavage total and differential cell count

Fig. 11


BAL(x 10 6)/Animal
0
5
10
15
20
25
30
35
100
50
10
100
50
10
pCT0129:lipid
pIN0773:lipid
OA/Dex
OA
No Chal
Macrophages
Eosinophils
Neutrophils
Lymphocytes
Total BAL Cells